

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.
 <120> Melanin Concentrating Hormone Antagonist
 <130> 2648W00P
 <150> JP 11-266298
 <151> 1999-09-20
 <150> JP 11-357889
 <151> 1999-12-16
 <150> JP 2000-126272
 <151> 2000-04-20
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<211> 353

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<213> Rat

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Met Asp Leu Gln Thr Ser Leu Leu Ser Thr Gly Pro Asn Ala Ser Asn

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Ile Ser Asp Gly Gln Asp Asn Leu Thr Leu Pro Gly Ser Pro Pro Arg

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Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly

35 40 45

Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala

50 55 60

Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile

65 70 75 80

Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met

85 90 95

Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly

100 105 110

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe

115 120 125

Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala

130 135 140

Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala

145 150 155 160

Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr

165 170 175

Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val

180 185 190

Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe

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195	200	205
Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile		
210	215	220
Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala		
225	230	235
Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg		
245	250	255
Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr		
260	265	270
Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr		
275	280	285
Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser		
290	295	300
Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys		
305	310	315
Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr		
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Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly		
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Thr

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<212> DNA

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ATCAACATCA TTATGCCTTC CGTGTTTGGT ACCATCTGTC TCCTGGGCAT CGTGGGAAAC	180
TCCACGGTCA TCTTTGCTGT GGTGAAGAAG TCCAAGCTAC ACTGGTGCAG CAACGTCCCC	240

GACATCTTCA TCATCAACCT CTCTGTGGTG GATCTGCTCT TCCTGCTGGG CATGCCTTTC 300
ATGATCCACC AGCTCATGGG GAACGGCGTC TGGCACTTTG GGGAAACCAT GTGCACCCTC 360
ATCACAGCCA TGGACGCCAA CAGTCAGTTC ACTAGCACCT ACATCCTGAC TGCCATGACC 420
ATTGACCGCT ACTTGGCCAC CGTCCACCCC ATCTCCTCCA CCAAGTCCG GAAGCCCTCC 480
ATGGCCACCC TGGTGATCTG CCTCCTGTGG GCGCTCTCCT TCATCAGTAT CACCCCTGTG 540
TGGCTCTACG CCAGGCTCAT TCCCTTCCCA GGGGGTGCTG TGGGCTGTGG CATCCGCCTG 600
CCAAACCCGG AACTGACCT CTACTGGTTC ACTCTGTACC AGTTTTCTCT GGCCTTTGCC 660
CTTCCGTTTG TGGTCATTAC CGCCGCATAC GTGAAAATAC TACAGCGCAT GACGTCTTCG 720
GTGGCCCCAG CCTCCCAACG CAGCATCCGG CTTCGGACAA AGAGGGTGAC CCGCACGGCC 780
ATTGCCATCT GTCTGGTCTT CTTTGTGTGC TGGGCACCCT ACTATGTGCT GCAGCTGACC 840
CAGCTGTCCA TCAGCCGCCC GACCCTCAGG TTTGTCTACT TGTACAACGC GGCCATCAGC 900
TTGGGCTATG CTAACAGCTG CCTGAACCCC TTTGTGTACA TAGTGCTCTG TGAGACCTTT 960
CGAAAACGCT TGGTGTGTC AGTGAAGCCT GCAGCCCAGG GGCAGCTCCG CACGGTCAGC 1020
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<213> Rat

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AUCAGCUGUC UGAGCGUUGC UGACCGUGCG GAGCUGCCCC UGGGCUGCAG GCUUCACUGA 180
CAACACCAAG CGUUUUCGAA AGGUCUCACA GAGCACUAUG UACACAAAGG GGUUCAGGCA 240
GCUGUUAGCA UAGCCCAAGC UG 262

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<213> Artificial Sequence

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CAACAGCTGC CTCAACCC 18

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<211> 18

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GGACAAGGTG GCAGGCGCTG GAGGCTGCCG CAGCCTGCGT GGGTGGAGGG GAGCTCAGCT 180
CGGTTGTGGG AGCAGGCGAC CGGCACTGGC TGGATGGACC TGGAAGCCTC GCTGCTGCCC 240
ACTGGTCCCA ACGCCAGCAA CACCTCTGAT GGCCCCGATA ACCTCACTTC GGCAGGATCA 300
CCTCCTCGCA CGGGGAGCAT CTCCTACATC AACATCATCA TGCCTTCGGT GTTCGGCACC 360
ATCTGCCTCC TGGGCATCAT CGGGAActCC ACGGTCATCT TCGCGGTCGT GAAGAAGTCC 420
AAGCTGCACT GGTGCAACAA CGTCCCCGAC ATCTTCATCA TCAACCTCTC GGTAGTAGAT 480
CTCCTCTTTC TCCTGGGCAT GCCCTTCATG ATCCACCAGC TCATGGGCAA TGGGGTGTGG 540
CACTTTGGGG AGACCATGTG CACCCTCATC ACGGCCATGG ATGCCAATAG TCAGTTCACC 600
AGCACCTACA TCCTGACCGC CATGGCCATT GACCGCTACC TGGCCACTGT CCACCCCATC 660
TCTTCCACGA AGTTCCGGAA GCCCTCTGTG GCCACCCTGG TGATCTGCCT CCTGTGGGCC 720
CTCTCCTTCA TCAGCATCAC CCCTGTGTGG CTGTATGCCA GACTCATCCC CTTCCCAGGA 780

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GGTGCAGTGG GCTGCGGCAT ACGCCTGCCC AACCCAGACA CTGACCTCTA CTGGTTCACC 840
 CTGTACCACT TTTTCCTGGC CTTTGCCCTG CCTTTTGTGG TCATCACAGC CGCATACGTG 900
 AGGATCCTGC AGCGCATGAC GTCCTCAGTG GCCCCGCCT CCCAGCGCAG CATCCGGCTG 960
 CGGACAAAGA GGGTGACCCG CACAGCCATC GCCATCTGTC TGGTCTTCTT TGTGTGCTGG 1020
 GCACCCTACT ATGTGCTACA GCTGACCCAG TTGTCCATCA GCCGCCCCGAC CCTCACCTTT 1080
 GTCTACTTAT ACAATGCGGC CATCAGCTTG GGCTATGCCA ACAGCTGCCT CAACCCCTTT 1140
 GTGTACATCG TGCTCTGTGA GACGTTCCGC AAACGCTTGG TCCTGTCGGT GAAGCCTGCA 1200
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<210> 9

<211> 422

<212> PRT

<213> Human

<400> 9

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 35 40 45
 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
 50 55 60
 Thr Gly Thr Gly Trp MeT Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
 65 70 75 80
 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
 85 90 95
 Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile MeT
 100 105 110
 Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser

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115	120	125
Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn		
130	135	140
Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu		
145	150	155
Phe Leu Leu Gly MeT Pro Phe MeT Ile His Gln Leu MeT Gly Asn Gly		
165	170	175
Val Trp His Phe Gly Glu Thr MeT Cys Thr Leu Ile Thr Ala MeT Asp		
180	185	190
Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala MeT Ala Ile		
195	200	205
Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg		
210	215	220
Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser		
225	230	235
Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe		
245	250	255
Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr		
260	265	270
Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu		
275	280	285
Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg MeT		
290	295	300
Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr		
305	310	315
Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val		
325	330	335
Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser		
340	345	350

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Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu

355

360

365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys

370

375

380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln

385

390

395

400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg

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415

Thr Glu Ser Lys Gly Thr

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<210> 12

<211> 33

<212> DNA

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<213> Artificial Sequence

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<400> 12

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<212> DNA

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<211> 1074

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<213> Human

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ATCAACATCA TCATGCCTTC GGTGTTCCGC ACCATCTGCC TCCTGGGCAT CATCGGGAAC 180
TCCACGGTCA TCTTCGCGGT CGTGAAGAAG TCCAAGCTGC ACTGGTGCAA CAACGTCCCC 240
GACATCTTCA TCATCAACCT CTCGGTAGTA GATCTCCTCT TTCTCCTGGG CATGCCCTTC 300
ATGATCCACC AGCTCATGGG CAATGGGGTG TGGCACTTTG GGGAGACCAT GTGCACCCTC 360
ATCACGGCCA TGGATGCCAA TAGTCAGTTC ACCAGCACCT ACATCCTGAC CGCCATGGCC 420
ATTGACCGCT ACCTGGCCAC TGTCCACCCC ATCTCTTCCA CGAAGTTCCG GAAGCCCTCT 480
GTGGCCACCC TGGTGATCTG CCTCCTGTGG GCCCTCTCCT TCATCAGCAT CACCCCTGTG 540
TGGCTGTATG CCAGACTCAT CCCCTTCCCA GGAGGTGCAG TGGGCTGCGG CATACGCCTG 600
CCCAACCCAG AACTGACCT CTA CTGTTT ACCCTGTACC AGTTTTTCCT GGCCTTTGCC 660

CTGCCTTTTG TGGTCATCAC AGCCGCATAC GTGAGGATCC TGCAGCGCAT GACGTCCTCA 720
GTGGCCCCCG CCTCCCAGCG CAGCATCCGG CTGCGGACAA AGAGGGTGAC CCGCACAGCC 780
ATCGCCATCT GTCTGGTCTT CTTTGTGTGC TGGGCACCCT ACTATGTGCT ACAGCTGACC 840
CAGTTGTCCA TCAGCCGCCC GACCCTCACC TTTGTCTACT TATACAATGC GGCCATCAGC 900
TTGGGCTATG CCAACAGCTG CCTCAACCCC TTTGTGTACA TCGTGCTCTG TGAGACGTTT 960
CGCAAACGCT TGGTCCTGTC GGTGAAGCCT GCAGCCCAGG GGCAGCTTCG CGCTGTCAGC 1020
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<212> DNA

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GGGACAAGGT GGCAGGCGCT GGAGGCTGCC GCAGCCTGCG TGGGTGGAGG GGAGCTCAGC 180
TCGGTTGTGG GAGCAGGCGA CCGGCACTGG CTGGATGGAC CTGGAAGCCT CGCTGCTGCC 240
CACTGGTCCC AACGCCAGCA ACACCTCTGA TGGCCCCGAT AACCTCACTT CGGCAGGATC 300
ACCTCCTCGC ACGGGGAGCA TCTCCTACAT CAACATCATC ATGCCTTCGG TGTTCCGGAC 360
CATCTGCCTC CTGGGCATCA TCGGGAATC CACGGTCATC TTCGCGGTG TGAAGAAGTC 420
CAAGCTGCAC TGGTGCAACA ACGTCCCCGA CATCTTCATC ATCAACCTCT CGGTAGTAGA 480
TCTCCTCTTT CTCCTGGGCA TGCCCTTCAT GATCCACCAG CTCATGGGCA ATGGGGTGTG 540
GCACTTTGGG GAGACCATGT GCACCCTCAT CACGGCCATG GATGCCAATA GTCAGTTCAC 600
CAGCACCTAC ATCCTGACCG CCATGGCCAT TGACCGCTAC CTGGCCACTG TCCACCCCAT 660
CTCTTCCACG AAGTTCCGGA AGCCCTCTGT GGCCACCCTG GTGATCTGCC TCCTGTGGGC 720
CCTCTCCTTC ATCAGCATCA CCCCTGTGTG GCTGTATGCC AGACTCATCC CCTTCCCAGG 780
AGGTGCAGTG GGCTGCGGCA TACGCCTGCC CAACCCAGAC ACTGACCTCT ACTGGTTTAC 840
CCTGTACCAG TTTTTCCTGG CCTTTGCCCT GCCTTTTGTG GTCATCACAG CCGCATACGT 900
GAGGATCCTG CAGCGCATGA CGTCCTCAGT GGCCCCGCC TCCCAGCGCA GCATCCGGCT 960
GCGGACAAAG AGGGTGACCC GCACAGCCAT CGCCATCTGT CTGGTCTTCT TTGTGTGCTG 1020

GGCACCCTAC TATGTGCTAC AGCTGACCCA GTTGTCCATC AGCCGCCCGA CCCTCACCTT 1080
TGTCTACTTA TACAATGCGG CCATCAGCTT GGGCTATGCC AACAGCTGCC TCAACCCCTT 1140
TGTGTACATC GTGCTCTGTG AGACGTTCCG CAAACGCTTG GTCCTGTCGG TGAAGCCTGC 1200
AGCCCAGGGG CAGCTTCGCG CTGTCAGCAA CGCTCAGACG GCTGACGAGG AGAGGACAGA 1260
AAGCAAAGGC ACCTGAACTA GTT 1283

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<213> Human

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GCUGCAGGCU UCACCGACAG GACCAAGCGU UUGCGGAACG UCUCACAGAG CACGAUGUAC 180
ACAAAGGGGU UGAGGCAGCU GUUGGCAUAG CCCAAGCUGA UGGCCGCAUU GUAUAAGUAG 240
ACAAAGGUGA GGGUCGGGCG GCUGAUGGAC AACUGGGUCA GCUGUAGCAC AUAGUAGGGU 300
GCCCAGCACA CAAAGAAGAC CAGACAGAU GCGAUGGCUG UGCGGGUCAC CCUCUUUGUC 360
CGCAGCCGGA UGCUGCGCUG GGAGGCGGGG GCCACUGAGG ACGUCAUGCG CUGCAGGAUC 420